



SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
KORNBLUTH, Richard S.

<120> MULTIMERIC FUSION PROTEINS OF TNF SUPERFAMILY LIGANDS (AMENDED)

<130> UCSD1590

<140> US 09/454,223
<141> 1999-12-09

<150> US 60/111,471
<151> 1998-12-09

<160> 22

<170> PatentIn version 3.1

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<223> Murine surfactant protein D (without the CRD) fused to the
extracellular portion of human CD40L

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<223> Signal peptide from murine surfactant protein D

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<223> Mature murine surfactant protein D including hub region,
collagenous portion, and neck, but excluding carbohydrate
recognition domain (CRD)

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<222> (801)..(1546)
<223> Human CD40 ligand extracellular region, including stalk.

<300>
<301> Motwani M
<302> Mouse surfactant protein-D. cDNA cloning, characterization, and
gene localization to chromosome 14.
<303> J. Immunol.
<304> 155
<305> 12

<306> 5671 TO 5677
 <307> 1995
 <313> (32)..(802)

<300>
 <301> Spriggs MK
 <302> Recombinant human CD40 ligand stimulates B cell proliferation and
 immunoglobulin E secretion
 <303> Journal of Experimental Medicine
 <304> 176
 <305> 6
 <306> 1543-1550
 <307> 1992
 <313> (803)..(1552)

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<303> Journal of Immunology
<304> 155
<305> 12
<306> 5671-5677
<307> 1995
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<300>
<301> Anderson, DM
<302> A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function.
<303> Nature
<304> 390
<305> 6656
<306> 175-179
<307> 1997
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<301> Motwani M
<302> Mouse surfactant protein-D. cDNA clonings, characterization, and
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<303> Nature
<304> 357
<305> 6373
<306> 80 TO 82
<307> 1992-05-07
<313> (801)..(1441)

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<301> Armitage RJ
<302> Molecular and biological characterization of a murine ligand for
      CD40.
<303> Nature
<304> 357
<305> 6373
<306> 80 TO 82
<307> 1992-05-07
<313> (801)..(1441)

<400> 5
gctagcgaat tccaccagga agcaatctga c atg ctg ccc ttt ctc tcc atg      52
      Met Leu Pro Phe Leu Ser Met
      1                      5

ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag      100
Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
      10                      15                      20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt      148
Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
      25                      30                      35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga      196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
      40                      45                      50                      55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg      244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
      60                      65                      70

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ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga	292
Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly	
75 80 85	
gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta	340
Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu	
90 95 100	
agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa	388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu	
105 110 115	
ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt	436
Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly	
120 125 130 135	
cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg	484
Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met	
140 145 150	
caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga	532
Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg	
155 160 165	
ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga	580
Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly	
170 175 180	
cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc	628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro	
185 190 195	
cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa	676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys	
200 205 210 215	
ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag	724
Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu	
220 225 230	
gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat	772
Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr	
235 240 245	
cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc	820
Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val	
250 255 260	
gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta	868
Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu	
265 270 275	
aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag	916
Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu	
280 285 290 295	
gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac	964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn	
300 305 310	

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aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag      1012
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
      315                      320                      325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca      1060
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala
      330                      335                      340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc      1108
Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
      345                      350                      355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa      1156
Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
      360                      365                      370                      375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag      1204
Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
      380                      385                      390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc      1252
Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
      395                      400                      405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc      1300
Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
      410                      415                      420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa      1348
Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
      425                      430                      435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa      1396
Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
      440                      445                      450                      455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc      1441
Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
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<400> 6

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Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
20           25           30

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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
 35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
 50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
 65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
 85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
 100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
 115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
 130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
 145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
 165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
 180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
 195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
 210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
 225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
 245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
 260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser

275 280 285
 Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
 290 295 300
 Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
 305 310 315 320
 Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
 325 330 335
 Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
 340 345 350
 Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
 355 360 365
 Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
 370 375 380
 Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
 385 390 395 400
 Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
 405 410 415
 Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
 420 425 430
 His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
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 Phe Gly Leu Leu Lys Leu
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<400> 15
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<220>
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 1 5 10 15

<210> 18
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<400> 20
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 <212> PRT
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 <223> Fusion sequence of SPD and RANKL/TRANCE sequence region

<400> 22

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